

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Nucleic acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

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<150> DE-198 19 829.9

<151> 1998-05-04

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Drosophila melanogaster

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<222> (372) .. (2681)

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aatttcgtaa gattagttgg tattaagggc agcccatgca cacagctaaa aagggaacta 240

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aattatatta ttgtaatcta gtagagagca gacaacatat ccgctggcaa caaccaacac 360

cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat 410

Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp

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gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458

Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe

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Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn

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cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554

Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His

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agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602

Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala

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tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650

Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln

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Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr

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Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro

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Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg

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Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met

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Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His

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 Val Leu Leu Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg
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 Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile
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tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc agc 1178
 Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser
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 Ser Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn
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 Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu
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 Asp Leu Leu Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu
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ctg gag tgg aac gac atg aat ctc cgc tgg aac acc tcc gac tat ggc 1514
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Phe Gln Leu Asp Leu Gln Leu Gln Asp Glu Thr Gly Gly Asp Ile Ser

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Ser Tyr Val Leu Asn Gly Glu Trp Glu Leu Leu Gly Val Pro Gly Lys

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Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile

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Leu Ile Ile Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe

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acc ctg ccg cca gat tcg ggt gaa aaa tta tcg ctg ggt gtt acc atc 2042

Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile

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Leu Glu Phe Pro Thr Thr Pro Cys Ser Asp Thr Ser Ser Glu Arg Lys

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His Gln Ile Leu Ser Asp Val Glu Leu Lys Glu Arg Ser Ser Lys Ser

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Thr Met Phe Ala Ile Leu Ala Thr Ile Ala Val Leu Leu Ser Ala Pro

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765

cat att att gtc tcg tagccatattg ggcgaggtgg ttattgttat tggttttatt 2721

His Ile Ile Val Ser

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gcggcgcgcg gcgcggcggc gtcgcggcgc tgac atg ggc ggg cgg gcg cgc cgc 355

Met Gly Gly Arg Ala Arg Arg

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Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Cys Leu Leu

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Tyr Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His

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cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499

His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu

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agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547

Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile

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gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595

Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys

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Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Phe Gly

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gtc ctt atg tac aac agc gcg gac gaa ggg ttc gac agc acg tat cca 739

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 Ser Phe Val Thr Asn Gly Glu Trp Glu Leu Ile Gly Val Pro Gly Lys
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 Thr Phe Ala Val Val Ile Arg Arg Lys Thr Leu Tyr Tyr Phe Phe Asn
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 Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile
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 tta ctg tcg ttg acg gtg ttc ctc aac atg gtg gcg gag acg atg cca 1219

Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro

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Ala Thr Ser Asp Ala Val Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile

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atg ttc atg gtg gct tcc tcc gtc gtc tcc acc ata ctg atc ctc aac 1315

Met Phe Met Val Ala Ser Ser Val Val Ser Thr Ile Leu Ile Leu Asn

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tac cac cac cgg cac gca gac act cac gaa atg agt gat tgg att cgt 1363

Tyr His His Arg His Ala Asp Thr His Glu Met Ser Asp Trp Ile Arg

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Cys Val Phe Leu Tyr Trp Leu Pro Trp Val Leu Arg Met Ser Arg Pro

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Leu Glu Leu Arg Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu

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Asp Ile Asp Asp Asp Phe Arg His Pro Gln Ala Gln Gln Pro Gln Cys

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 Cys Arg Tyr Tyr Arg Gly Gly Glu Glu Asn Gly Ala Gly Leu Ala Ala

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 His Ser Cys Phe Gly Val Asp Tyr Glu Leu Ser Leu Ile Leu Lys Glu

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Met Ala Pro Met Leu Ala Ala

1

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Leu Ala Leu Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu

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aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211

Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg

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ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259

Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr

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ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307

Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr

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aat ata tgg ctg tct ttg gag tgg aat gac tac aac ctg agg tgg aac 355

Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn

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gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag 403

Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys

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ttg tgg aag ccg gac gtc ctt atg tat aat agt gct gac gag ggt ttt 451

Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe

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ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc 547

Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile

140

145

150

gcg tgg ttc ccc ttc gac gac caa cac tgt gat atg aag ttc ggt agc 595

Ala Trp Phe Pro Phe Asp Asp Gln His Cys Asp Met Lys Phe Gly Ser

155

160

165

tgg aca tat gac ggc aat cag ttg gat ctg gtg cta aaa gat gag gca 643

Trp Thr Tyr Asp Gly Asn Gln Leu Asp Leu Val Leu Lys Asp Glu Ala

170

175

180

ggc ggc gat cta tcg gac ttc ata aca aat ggg gag tgg tat cta ata 691

Gly Gly Asp Leu Ser Asp Phe Ile Thr Asn Gly Glu Trp Tyr Leu Ile

185

190

195

gga atg cca ggc aaa aag aac aca ata aca tac gcg tgc tgc ccc gag 739

Gly Met Pro Gly Lys Lys Asn Thr Ile Thr Tyr Ala Cys Cys Pro Glu

200

205

210

215

ccc tac gtg gac gtc acc ttc acc atc atg ata aga aga cga acc ttg 787

Pro Tyr Val Asp Val Thr Phe Thr Ile Met Ile Arg Arg Arg Thr Leu

220

225

230

tac tac ttc ttc aac ctg atc gtc ccg tgc gtg ctg atc tca tcg atg 835

Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ser Ser Met

235

240

245

gca ctc ctc ggc ttc aca ctg cca cca gac tcc gga gag aaa ctc aca 883

Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Thr

250

255

260

ctt gga gtc act att ctt cta tcg ctg acg gtg ttc ctc aac ctg gta 931

Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn Leu Val

265

270

275

gcc gag acc ctg cca cag gtc tcc gac gct atc ccc ctg tta ggg acg 979

Ala Glu Thr Leu Pro Gln Val Ser Asp Ala Ile Pro Leu Leu Gly Thr

280

285

290

295

tac ttc aat tgc atc atg ttc atg gta gcg tcg tct gtg gta ctg act 1027

Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val Leu Thr

300

305

310

gtg gtg gta ctc aat tac cac cat cga aca gct gat ata cat gaa atg 1075

Val Val Val Leu Asn Tyr His His Arg Thr Ala Asp Ile His Glu Met

315

320

325

cca cag tgg ata aaa tca gta ttc cta caa tgg ttg cca tgg ata ctg 1123

Pro Gln Trp Ile Lys Ser Val Phe Leu Gln Trp Leu Pro Trp Ile Leu

330

335

340

cga atg tcg agg cca ggg aag aag atc acc agg aag act ata atg atg 1171

Arg Met Ser Arg Pro Gly Lys Lys Ile Thr Arg Lys Thr Ile Met Met

345

350

355

aac acg agg atg agg gag ctg gaa ctg aag gag agg tcg tcg aag tcc 1219

Asn Thr Arg Met Arg Glu Leu Glu Leu Lys Glu Arg Ser Ser Lys Ser

360

365

370

375

ttg ctg gcg aat gtt cta gat att gat gat gac ttc aga cac ggc cct 1267

Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Gly Pro

380

385

390

ccg cct cct aac agt act gcc tcg acc ggg aat ttg gga cct ggg tgc 1315

Pro Pro Pro Asn Ser Thr Ala Ser Thr Gly Asn Leu Gly Pro Gly Cys

395

400

405

tca ata ttc cgc acg gat ttc cgt cgg tcg ttc gtc cgt ccg tcc acg 1363

Ser Ile Phe Arg Thr Asp Phe Arg Arg Ser Phe Val Arg Pro Ser Thr

410

415

420

atg gaa gac gtg ggc ggc ggg ctg ggt agc cac cat cgc gag ctg cac 1411

Met Glu Asp Val Gly Gly Gly Leu Gly Ser His His Arg Glu Leu His

435

455

470

485

500

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3109